

- (iii) NUMBER OF SEQUENCES: 11

- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Limbach & Limbach
 - (B) STREET: 2001 Ferry Building
 - (C) CITY: San Francisco
 - (D) STATE: CAL
 - (F) ZIP: 94111

- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent in Release #1.0, Version #1.25

- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 923,692
 - (B) FILING DATE: 31-JUL-1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 600,244
 - (B) FILING DATE: 22-OCT-1990

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 641,617
 - (B) FILING DATE: 16-JAN-1991

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 310,881
 - (B) FILING DATE: 17-FEB-1989

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 160,766
 - (B) FILING DATE: 26-FEB-1988

- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 160,771

(B) FILING DATE: 26-FEB-1988

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 347,637

(B) FILING DATE: 05-MAY-1989

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 363,138

(B) FILING DATE: 08-JUN-1989

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 219,279

(B) FILING DATE: 15-JUL-1988

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Halluin, Albert P.

(B) REGISTRATION NUMBER: 28,957

(C) REFERENCE/DOCKET NUMBER: BIOG-20121 USA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-433-4150

(B) TELEFAX: 415-433-8716

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Pro Xaa Gly Pro

1

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGGTACCTGG GCC

13

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 886 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Chinese cucumber
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: alpha-trichosanthin
- (ix) FEATURE:
 - (A) NAME/KEY: CDS (B) LOCATION: 8. .877
 - (B) LOCATION: 8. .877
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGAGG ATG ATC AGA TTC TTA GTC CTC TCT TTG CTA ATT CTC ACC CTC	49
Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu	
1 5 10	
TTC CTA ACA ACT CCT GCT GTG GAG GGC GAT GTT AGC TTC CGT TTA TCA	97
Phe Leu Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser	
15 20 25 30	
GGT GCA ACA AGC AGT TCC TAT GGA GTT TTC ATT TCA AAT CTG AGA AAA	145
Gly Ala Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys	
35 40 45	
GCT CTT CCA AAT GAA AGG AAA CTG TAC GAT ATC CCT CTG TTA CGT TCC	193
Ala Leu Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser	
50 55 60	

TCT CTT CCA GGT TCT CAA CGC TAC GCA TTG ATC CAT CTC ACA AAT TAC	241
Ser Leu Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr	
65 70 75	
GCC GAT GAA ACC ATT TCA GTG GCC ATA GAC GTA ACG AAC GTC TAT ATT	289
Ala Asp Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile	
80 85 90	
ATG GGA TAT CGC GCT GGC GAT ACA TCC TAT TTT TTC AAC GAG GCT TCT	337
Met Gly Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser	
95 100 105 110	
GCA ACA GAA GCT GCA AAA TAT GTA TTC AAA GAC GCT ATG CGA AAA GTT	385
Ala Thr Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val	
115 120 125	
ACG CTT CCA TAT TCT GGC AAT TAC GAA AGG CTT CAA ACT GCT GCG GGC	433
Thr Leu Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly	
130 135 140	
AAA ATA AGG GAA AAT ATT CCG CTT GGA CTC CCA GCT TTG GAC AGT GCC	481
Lys Ile Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala	
145 150 155	
ATT ACC ACT TTG TTT TAC TAC AAC GCC AAT TCT GCT GCG TCG GCA CTT	529
Ile Thr Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu	
160 165 170	

- 7 -

[illegible]

Tyr Ala Ile

290

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu Phe Leu
1 5 10 15

Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser Gly Ala
20 25 30

Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys Ala Leu
35 40 45

Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser Ser Leu
50 55 60

Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr Ala Asp
65 70 75 80

Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile Met Gly
85 90 95

Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser Ala Thr

100	105	110
Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val Thr Leu		
115	120	125
Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly Lys Ile		
130	135	140
Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala Ile Thr		
145	150	155 160
Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu Met Val		
165	170	175
Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile Glu Gln		
180	185	190
Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu Ala Ile		
195	200	205
Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile Gln Ile		
210	215	220
Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu Ile Asn		
225	230	235 240
Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly Val Val		
245	250	255
Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala Ala Met		
260	265	270
Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser Tyr Ala		
275	280	285

Ile

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Oryza sativa*
- (vii) IMMEDIATE SOURCE:
(B) CLONE: alpha-amylase
- (ix) FEATURE:
(A) NAME/KEY: CDS (B) LOCATION: 12..1316
(B) LOCATION: 12..1316
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCTCGAGGTG C ATG CAG GTG CTG AAC ACC ATG GTG AAC A CAC TTC TTG

48

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu

1

5

10

TCC CTT TCG GTC CTC ATC GTC CTC CTT GGC CTC TCC TCC AAC TTG ACA

96

Ser Leu Ser Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr

15	20	25	
GCC GGG CAA GTC CTG TTT CAG GGA TTC AAC TGG GAG TCG TGG AAG GAG			144
Ala Gly Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu			
30	35	40	45
AAT GGC GGG TGG TAC AAC TTC CTG ATG GGC AAG GTG GAC GAC ATC GCC			192
Asn Gly Gly Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala			
50	55	60	
GCA GCC GGC ATC ACC CAC GTC TGG CTC CCT CCG CCG TCT CAC TCT GTC			240
Ala Ala Gly Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val			
65	70	75	
GGC GAG CAA GGC TAC ATG CCT GGG CGG CTG TAC GAT CTG GAC GCG TCT			288
Gly Glu Gln Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser			
80	85	90	
AAG TAC GGC AAC GAG GCG CAG CTC AAG TCG CTG ATC GAG GCG TTC CAT			336
Lys Tyr Gly Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His			
95	100	105	
GGC AAG GGC GTC CAG GTG ATC GCC GAC ATC GTC ATC AAC CAC CGC ACG			384
Gly Lys Gly Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr			
110	115	120	125
GCG GAG CAC AAG GAC GGC CGC GGC ATC TAC TGC CTC TTC GAG GGC GGG			432
Ala Glu His Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly			
130	135	140	

ACG CCC GAC TCC CGC CTC GAC TGG GGC CCG CAC ATG ATC TGC CGC GAC	480
Thr Pro Asp Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp	
145 150 155	
GAC CCC TAC GGC CAT GGC ACC GGC AAC CCG GAC ACC GGC GCC GAC TTC	528
Asp Pro Tyr Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe	
160 165 170	
GCC GCC GCG CCG GAC ATC GAC CAC CTC AAC AAG CGC GTC CAG CGG GAG	576
Ala Ala Ala Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu	
175 180 185	
CTC ATT GGC TGG CTC GAC TGG CTC AAG ATG GAC ATC GGC TTC GAC GCG	624
Leu Ile Gly Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala	
190 195 200 205	
TGG CGC CTC GAC TTC GCC AAG GGC TAC TCC GCC GAC ATG GCA AAC ATC	672
Trp Arg Leu Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile	
210 215 220	
TAC ATC GAC GCC ACC GAG CCG AGC TTC GCC GTG CCC GAG ATA TCG ACG	720
Tyr Ile Asp Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr	
225 230 235	
TCC ATG GCG AAC GGC GGG GAC GGC AAG CCG AAC TAC GAC CAG AAC GCG	768
Ser Met Ala Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala	
240 245 250	

CAC CGG CAG GAG CTG GTC AAC TGG GTC GAT CGT GTC GGC GGC GCC AAC	816
His Arg Gln Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn	
255 260 265	
ACC AAC GGC ACG GCG TTC GAC TTC ACC ACC AAG GGC ATC CTC AAC GTC	864
Ser Asn Gly Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val	
270 275 280 285	
GCC GTG GAG GGC GAG CTG TGG CGC CTC CGC GGC GAG GAC GGC AAG GCG	912
Ala Val Glu Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala	
290 295 300	
CCC GGC ATG ATC GGG TGC TGG CCG GCC AAG GCG ACG ACC TTC GTC GAC	960
Pro Gly Met Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp	
305 310 315	
AAC CAC GAC ACC GGC TCG ACG CAG CAC CTG TGG CCG TTC CCC TCC GAC	1008
Asn His Asp Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp	
320 325 330	
AAG GTC ATG CAG GGC TAC GCA TAC ATC CTC ACC CAC CCC GGC AAC CCA	1056
Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro	
335 340 345	
TGC ATC TTG TAC GAC CAT TTC TTC GAT TGG GGT CTC AAG GAG GAG ATC	1104
Cys Ile Phe Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile	
350 355 360 365	
GAG CGC CTG GTG TCA ATC AGA AAC CGG CAG GGG ATC CAC CCG GCG AGC	1152

Glu Arg Leu Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser	
370 375 380	
GAG CTG CGC ATC ATG GAA GCT GAC AGC GAT CTC TAC CTC GCG GAG ATC	1200
Glu Leu Arg Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile	
385 390 395	
GAT GGC AAG GTG ATC ACA AAG ATT GGA CCA AGA TAC GAC GTC GAA CAC	1248
Asp Gly Lys Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His	
400 405 410	
CTC ATC CCC GAA GGC TTC CAG GTC GTC GCG CAC GGT GAT GGC TAC GCA	1296
Leu Ile Pro Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala	
415 420 425	
ATC TGG GAG AAA ATC TGAGCGCACG ATGACGAGAC TCTCAGTTTA GCAGATTTAA	1351
Ile Trp Glu Lys LIe	
430 435	
CCTGCGATTT TTACCCTGAC CGGTATACGT ATATACGTGC CGGCAACGAG CTGTATCCGA	1411
TCCGAATTAC GGATGCAATT GTCCACGAAG TCCTCGAGG	1450

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids

(B) TYPE: amino acid

(D) Topology: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Gln	Val	Leu	Asn	Thr	Met	Val	Asn	Lys	His	Phe	Leu	Ser	Leu	Ser
1				5					10					15	
Val	Leu	Ile	Val	Leu	Leu	Gly	Leu	Ser	Ser	Asn	Leu	Thr	Ala	Gly	Gln
			20					25					30		
Val	Leu	Phe	Gln	Gly	Phe	Asn	Trp	Glu	Ser	Trp	Lys	Glu	Asn	Gly	Gly
		35				40					45				
Trp	Tyr	Asn	Phe	Leu	Met	Gly	Lys	Val	Asp	Asp	Ile	Ala	Ala	Ala	Gly
	50					55					60				
Ile	Thr	His	Val	Trp	Leu	Pro	Pro	Pro	Ser	His	Ser	Val	Gly	Glu	Gln
65				70						75				80	
Gly	Tyr	Met	Pro	Gly	Arg	Leu	Tyr	Asp	Leu	Asp	Ala	Ser	Lys	Tyr	Gly
			85					90					95		
Asn	Glu	Ala	Gln	Leu	Lys	Ser	Leu	Ile	Glu	Ala	Phe	His	Gly	Lys	Gly
		100					105					110			
Val	Gln	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Thr	Ala	Glu	His
	115					120					125				
Lys	Asp	Gly	Arg	Gly	Ile	Tyr	Cys	Leu	Phe	Glu	Gly	Gly	Thr	Pro	Asp
	130				135					140					
Ser	Arg	Leu	Asp	Trp	Gly	Pro	His	Met	Ile	Cys	Arg	Asp	Asp	Pro	Tyr
145				150					155					160	

Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe Ala Ala Ala
165 170 175

Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu Leu Ile Gly
180 185 190

Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala Trp Arg Leu
195 200 205

Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile Tyr Ile Asp
210 215 220

Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr Ser Met Ala
225 230 235 240

Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala His Arg Gln
245 250 255

Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn Ser Asn Gly
260 265 270

Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val Ala Val Glu
275 280 285

Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala Pro Gly Met
290 295 300

Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp Asn His Asp
305 310 315 320

Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp Lys Val Met
325 330 335

Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro Cys Ile Phe
340 345 350

Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile Glu Arg Leu
355 360 365

Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser Glu Leu Arg
370 375 380

Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile Asp Gly Lys
385 390 395 400

Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His Leu Ile Pro
405 410 415

Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala Ile Trp Glu
420 425 430

Lys Ile

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (G) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: alpha-hemoglobin

(ix) FEATURE:

(A) NAME/KEY: transit_peptide (B) LOCATION: 26. .241

(B) LOCATION: 26. .241

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 245. .670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGAGGGCA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC AAGGGATACA	60
AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT CAAGTTTCT	120
TGTTTTTGGG TGTA AAAAAC TGAAAATTC AGCAAATTC ATGTTGGTTT TGAAAAAAGA	180
TTCAATTTTT ATGCAAAAGT TTTGTTCTT TAGGATTTCA GCAGGTGGTA GAGTTTCTTG	240
CATG GTG CTG TCT CCT GCC GAC AAG ACC AAC GTC AAG GCC GCC TGG GGC	289
Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Cly	
1 5 10 15	
AAG GTT GGC GCG CAC GCT GGC GAG TAT GGT GCG GAG GCC CTG GAG AGG	337
Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg	
20 25 30	
ATG TTC CTG TCC TTC CCC ACC ACC AAG ACC TAC TTC CCG CAC TTC GAC	385
Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp	
35 40 45	
CTG AGC CAC GGC TCT GCC CAG GTT AAG GGC CAC GGC AAG AAG GTG GCC	433

Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala
 50 55 60

GAC GCG CTG ACC AAC GCC GTG GCG CAC GTG GAC GAC ATG CCC AAC GCG 481

Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala
 65 70 75

CTG TCC GCC CTG AGC GAC CTG CAC GCG CAC AAG CTT CGG GTG GAC CCG 529

Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro
 80 85 90 95

GTC AAC TTC AAG CTC CTA AGC CAC TGC CTG CTG GTG ACC CTG GCC GCC 577

Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala
 100 105 110

CAC CTC CCC GCC GAG TTC ACC CCT GCG GTG CAC GCC TCC CTG GAC AAG 625

His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys
 115 120 125

TTC CTG GCT TCT GTG AGC ACC GTG CTG ACC TCC AAA TAC CGT TAAGCTGGAG 677

Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
 130 135 140

CCTCGGTAGC CGTTCCTCCT GCCCGGTCTGA CC 709

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys
1 5 10 15

Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
20 25 30

Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
35 40 45

Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
50 55 60

Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
65 70 75 80

Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
85 90 95

Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
100 105 110

Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
115 120 125

Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
 130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: beta-hemoglobin
- (ix) FEATURE:
 - (A) NAME/KEY: transit_peptide (B) LOCATION: 26..241
 - (B) LOCATION: 26..241
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 245..685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTCGAGGGGA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC AAGGGATACA

AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT CAAGTTTTCT 120

TGTTTTTGGA TCTAAAAAC TGAAAAATTC AGCAAATTCT ATGTTGGTTT TGAAAAAGA 180

TTCAATTTTT ATGCAAAGT TTTGTTTCCTT TAGGATTTC GCAGGTGGTA GAGTTTCTTG 240

GATG GTG CAC CTG ACT CCT GAG GAG AAG TCT GCC GTT ACT GCC CTG TGG 289

Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp
1 5 10 15

GGC AAG GTG AAC GTG GAT GAA GTT GGT GGT GAG GCC CTG GGC AGG CTG 337

Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
20 25 30

CTG GTG GTC TAC CCT TGG ACC CAG AGG TTC TTT GAG TCC TTT GGG GAT 385

Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp
35 40 45

CTG TCC ACT CCT GAT GCT GTT ATG GGC AAC CCT AAG GTG AAG GCT CAT 433

Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His
50 55 60

GGC AAG AAA GTG CTG GGT GCC TTT AGT GAT GGC CTG GCT CAC CTG GAC 481

Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp
65 70 75

AAC CTC AAG GGC ACC TTT GCC ACC CTG AGT GAG CTG CAC TGT GAC AAG 529

Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
80 85 90 95

CTG CAC GTG GAT CCT GAG AGC TTC AGG CTC CTA GGC AAC GTG CTG GTC 577

Leu His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val
100 105 110

TGT GTG CTG GCG CAT CAC TTT GGC AAA GAA TTC ACC CCA CCA GTG CAG 625

Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln
115 120 125

GCT GCC TAT CAG AAA GTG GTG GCT GGT GTG GCT AAT GCC CTG GCC CAC 673

Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His
130 135 140

AAG TAT CAC TAAGCTCGCT TTCTTGCTGT CCAATTTCTA TTAAAGGTTTC 722

Lys Tyr His
145

CTTTGTGGGG TCGAGGTCGA C 743

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly
1 5 10 15

Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
20 25 30

Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
35 40 45

Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
50 55 60

Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn
65 70 75 80

Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu
85 90 95

His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val Cys
100 105 110

Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
115 120 125

Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
130 135 140

Tyr His
145

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: alkalophilic Bacillus sp.
(B) STRAIN: 38-2

(vii) IMMEDIATE SOURCE:
(B) CLONE: beta-cyclodextrin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala	Pro	Asp	Thr	Ser	Val	Ser	Asn	Lys	Gln	Asn	Phe	Ser	Thr	Asp	Val
1				5				10						15	

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REMARKS

The present Amendment is in response to Examiner's Notice to Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures mailed April 8, 1993.

Applicants submit this Amendment to complete their disclosure of the sequences employed in the instant application pursuant to 37 C.F.R. § 1.821 et seq. Applicants also submit herewith a paper copy of the Sequence Listing and a floppy disk containing the Sequence Listing in computer readable form in compliance with 37 C.F.R. §§ 1.821 (c) and (e).

Examiner will note that no new matter has been introduced by the instant amendment to the Specification or by these submissions and that the content of the amendment to the Specification and the paper and computer readable copies of the Sequence

Listing are the same. Therefore, entry of the instant amendment is proper.

Respectfully submitted,

LIMBACH & LIMBACH

Dated: 7/28/83

By: Albert P. Halluin
Albert P. Halluin
Registration No. 25,227

Attorneys for Applicant